

Amendments to the Specification:

Please amend the paragraph at page 12, lines 8-18 as follows:

Factor V/VIII domains also have two conserved regions, which are different parts of a single, functional domain. Factor V/VIII domains occur in a wide range of proteins, where they are believed to function in cell adhesion and/or phospholipid binding. Many of the proteins that contain this domain are also involved in some neuronal functions. See, PROSITE: <http://www.expasy.ch/cgi-bin/nicedoc.pl?PDOC00988> [www.expasy.ch/cgi-bin/nicedoc.pl?PDOC00988](http://www.expasy.ch/cgi-bin/nicedoc.pl?PDOC00988). The first conserved region can be represented by the sequence motif [GAS]W<sub>x</sub>{7,15}[FYW][LIV]<sub>x</sub>[LIVFA][GSTDEN]<sub>xxxxxx</sub>[LIVF]<sub>xx</sub>[IV]<sub>x</sub>[LIVT][QKM]G (SEQ ID NO:10), corresponding to residues 298-331 of SEQ ID NO:2. The second conserved region can be represented by the sequence motif P<sub>x</sub>{8,10}[LM]R<sub>x</sub>[GE][LIVP]<sub>x</sub>GC (SEQ ID NO:11), corresponding to residues 396-412 of SEQ ID NO:2.

Please amend the paragraph at page 40, lines 24-29 as follows:

The present invention also provides reagents for use in diagnostic applications. For example, the zcub5 gene, a probe comprising zcub5 DNA or RNA, or a subsequence thereof can be used to determine the presence of mutations at or near the zcub5 locus at human chromosome 6q21. This region of chromosome 6 has been associated with retinitis pigmentosa. See, OMIM™ Database, Johns Hopkins University, 2000 (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=OMIM> [www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=OMIM](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=OMIM)).

Please amend the paragraph at page 42, lines 10-20 as follows:

Sequence tagged sites (STSs) can also be used independently for chromosomal localization. An STS is a DNA sequence that is unique in the human genome and can be used as a reference point for a particular chromosome or region of a chromosome. An STS is defined by a pair of oligonucleotide primers that are used in a polymerase chain reaction to specifically detect this site in the presence of all other genomic sequences. Since STSs are based solely on DNA sequence they can be completely described within an electronic database, for example, Database of Sequence Tagged Sites (dbSTS), GenBank (National Center for Biological Information, National Institutes of Health, Bethesda, MD <http://www.ncbi.nlm.nih.gov> [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov)), and can be searched with a gene sequence of interest for the mapping data contained within these short genomic landmark STS sequences.